



#4

SEQUENCE LISTING

<110> BROWN, Eric L.
LEE, Lawrence
HOOK, Magnus

<120> METHOD OF PREVENTING T CELL-MEDIATED RESPONSES BY THE USE OF THE MAJOR HISTOCOMPATIBILITY COMPLEX CLASS II ANALOG PROTEIN (MAP PROTEIN) FROM STAPHYLOCOCCUS AUREUS

<130> P07023US01/BAS

<140> 10/041,775

<141> 2002-01-10

<150> 60/260,523

<151> 2001-01-10

<160> 4

<170> PatentIn version 3.1

<210> 1

<211> 603

<212> DNA

<213> Staphylococcus aureus

<220>

<221> CDS

<222> (1)..(603)

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aca	atc	act	gtg	aat	ggt	aca	agc	caa	aac	att	tta	tca	agc	tta	aca	96
Thr	Ile	Thr	Val	Asn	Gly	Thr	Ser	Gln	Asn	Ile	Leu	Ser	Ser	Leu	Thr	
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ttt	aat	aag	aat	caa	caa	att	agt	tat	aaa	gat	ata	gag	aat	aaa	gtt	144
Phe	Asn	Lys	Asn	Gln	Gln	Ile	Ser	Tyr	Lys	Asp	Ile	Glu	Asn	Lys	Val	
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aaa	tca	gtt	tta	tac	ttt	aat	aga	ggt	att	agt	gat	atc	gat	tta	aga	192
Lys	Ser	Val	Leu	Tyr	Phe	Asn	Arg	Gly	Ile	Ser	Asp	Ile	Asp	Leu	Arg	
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ctt	tct	aag	caa	gca	aaa	tac	acg	gtt	cat	ttt	aag	aat	gga	aca	aaa	240
Leu	Ser	Lys	Gln	Ala	Lys	Tyr	Thr	Val	His	Phe	Lys	Asn	Gly	Thr	Lys	
65					70					75					80	

aga	gtt	gtc	gat	ttg	aaa	gca	ggc	att	cac	aca	gcc	gac	tta	atc	aat	288
Arg	Val	Val	Asp	Leu	Lys	Ala	Gly	Ile	His	Thr	Ala	Asp	Leu	Ile	Asn	
				85					90						95	

aca agt gac att aaa gca att agt gtt aac gta gat act aaa aag caa	336
Thr Ser Asp Ile Lys Ala Ile Ser Val Asn Val Asp Thr Lys Lys Gln	
100 105 110	

gtg aaa gat aaa gag gca aaa gca aat gtt caa gtg ccg tat aca atc	384
Val Lys Asp Lys Glu Ala Lys Ala Asn Val Gln Val Pro Tyr Thr Ile	
115 120 125	

act gtg aat ggt aca agc caa aac att tta tca aac tta aca ttt aaa	432
Thr Val Asn Gly Thr Ser Gln Asn Ile Leu Ser Asn Leu Thr Phe Lys	
130 135 140	

aag aat cag caa att agt tat aaa gat tta gag aat aat gta aaa tca	480
Lys Asn Gln Gln Ile Ser Tyr Lys Asp Leu Glu Asn Asn Val Lys Ser	
145 150 155 160	

gtt tta aaa tca aac aga ggt ata act gat gta gat tta aga ctt tca	528
Val Leu Lys Ser Asn Arg Gly Ile Thr Asp Val Asp Leu Arg Leu Ser	
165 170 175	

aaa caa gcg aaa ttt aca gtt aat ttt aaa aat ggc acg aaa aaa gtt	576
Lys Gln Ala Lys Phe Thr Val Asn Phe Lys Asn Gly Thr Lys Lys Val	
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atc gat ttg aaa gca ggc att tat tga	603
Ile Asp Leu Lys Ala Gly Ile Tyr	
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Thr Ile Thr Val Asn Gly Thr Ser Gln Asn Ile Leu Ser Ser Leu Thr
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Phe Asn Lys Asn Gln Gln Ile Ser Tyr Lys Asp Ile Glu Asn Lys Val
35 40 45

Lys Ser Val Leu Tyr Phe Asn Arg Gly Ile Ser Asp Ile Asp Leu Arg
50 55 60

Leu Ser Lys Gln Ala Lys Tyr Thr Val His Phe Lys Asn Gly Thr Lys
65 70 75 80

Arg Val Val Asp Leu Lys Ala Gly Ile His Thr Ala Asp Leu Ile Asn
85 90 95

Thr Ser Asp Ile Lys Ala Ile Ser Val Asn Val Asp Thr Lys Lys Gln
100 105 110

Val Lys Asp Lys Glu Ala Lys Ala Asn Val Gln Val Pro Tyr Thr Ile
115 120 125

Thr Val Asn Gly Thr Ser Gln Asn Ile Leu Ser Asn Leu Thr Phe Lys
130 135 140

Lys Asn Gln Gln Ile Ser Tyr Lys Asp Leu Glu Asn Asn Val Lys Ser
145 150 155 160

Val Leu Lys Ser Asn Arg Gly Ile Thr Asp Val Asp Leu Arg Leu Ser
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180 185 190

Ile Asp Leu Lys Ala Gly Ile Tyr
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<221> CDS
<222> (1)..(396)
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Thr Ile Thr Val Asn Gly Thr Ser Gln Asn Ile Leu Ser Ser Leu Thr
20 25 30

ttt aat aag aat caa caa att agt tat aaa gat ata gag aat aaa gtt 144
Phe Asn Lys Asn Gln Gln Ile Ser Tyr Lys Asp Ile Glu Asn Lys Val
35 40 45

aaa tca gtt tta tac ttt aat aga ggt att agt gat atc gat tta aga 192

Lys	Ser	Val	Leu	Tyr	Phe	Asn	Arg	Gly	Ile	Ser	Asp	Ile	Asp	Leu	Arg		
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Leu	Ser	Lys	Gln	Ala	Lys	Tyr	Thr	Val	His	Phe	Lys	Asn	Gly	Thr	Lys		
65					70				75						80		
aga	gtt	gtc	gat	ttg	aaa	gca	ggc	att	cac	aca	gcc	gac	tta	atc	aat	288	
Arg	Val	Val	Asp	Leu	Lys	Ala	Gly	Ile	His	Thr	Ala	Asp	Leu	Ile	Asn		
				85					90					95			
aca	agt	gac	att	aaa	gca	att	agt	gtt	aac	gta	gat	act	aaa	aag	caa	336	
Thr	Ser	Asp	Ile	Lys	Ala	Ile	Ser	Val	Asn	Val	Asp	Thr	Lys	Lys	Gln		
			100					105					110				
gtg	aaa	gat	aaa	gag	gca	aaa	gca	aat	gtt	gtc	gac	ctg	cag	cca	agc	384	
Val	Lys	Asp	Lys	Glu	Ala	Lys	Ala	Asn	Val	Val	Asp	Leu	Gln	Pro	Ser		
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tta	att	agc	tga													396	
Leu	Ile	Ser															
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<210> 4
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Thr	Ile	Thr	Val	Asn	Gly	Thr	Ser	Gln	Asn	Ile	Leu	Ser	Ser	Leu	Thr		
			20					25					30				
Phe	Asn	Lys	Asn	Gln	Gln	Ile	Ser	Tyr	Lys	Asp	Ile	Glu	Asn	Lys	Val		
		35					40					45					
Lys	Ser	Val	Leu	Tyr	Phe	Asn	Arg	Gly	Ile	Ser	Asp	Ile	Asp	Leu	Arg		
		50				55					60						
Leu	Ser	Lys	Gln	Ala	Lys	Tyr	Thr	Val	His	Phe	Lys	Asn	Gly	Thr	Lys		
65					70				75						80		
Arg	Val	Val	Asp	Leu	Lys	Ala	Gly	Ile	His	Thr	Ala	Asp	Leu	Ile	Asn		
				85					90					95			
Thr	Ser	Asp	Ile	Lys	Ala	Ile	Ser	Val	Asn	Val	Asp	Thr	Lys	Lys	Gln		
			100					105					110				

Val Lys Asp Lys Glu Ala Lys Ala Asn Val Val Asp Leu Gln Pro Ser
115 120 125

Leu Ile Ser
130